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 3 <110> APPLICANT: ITOH, Kyogo et al.
 5 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN SART-13 AND TUMOR ANTIGEN
PEPTIDES THEREOF
 7 <130> FILE REFERENCE: 0020-4817P
 9 <140> CURRENT APPLICATION NUMBER: 09/763,985A
10 <141> CURRENT FILING DATE: 2001-02-28
12 <160> NUMBER OF SEQ ID NOS: 64
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 3798
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (12)..(2900)
24 <223> OTHER INFORMATION:
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32 gct gag tcc aag gct ggg ccc aag gct gac gga gag gag gat gag gtt      98
33 Ala Glu Ser Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val
34     15                  20                  25
36 aag gcg gct agg aca agg aga aag gtg tta tcg cgg gct gtg gcc gct      146
37 Lys Ala Ala Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala
38 30                  35                  40                  45
40 gcg aca tac aag acc atg ggg cca gcg tgg gat cag cag gag gaa ggc      194
41 Ala Thr Tyr Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly
42                 50                  55                  60
44 gtg agc gag agc gat ggg gat gag tac gcc atg gct tcc tcc gcg gag      242
45 Val Ser Glu Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu
46             65                  70                  75
48 agc tcc ccc ggg gag tac gag tgg gaa tat gac gaa gag gag gag aaa      290
49 Ser Ser Pro Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys
50         80                  85                  90
52 aac cag ctg gag att gag aga ctg gag gag cag ttg tct atc aac gtc      338
53 Asn Gln Leu Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val
54     95                  100                 105
56 tat gac tac aac tgc cat gtg gac ttg atc aga ctg ctc agg ctg gaa      386
57 Tyr Asp Tyr Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu
58 110             115                 120                 125
60 ggg gag ctt acc aag gtg agg atg gcc cgc cag aag atg agt gaa atc      434
61 Gly Glu Leu Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile
62             130                 135                 140
64 ttt ccc ttg act gaa gag ctc tgg ctg gag tgg ctg cat gac gag atc      482
65 Phe Pro Leu Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile
66             145                 150                 155
68 agc atg gcc cag gat ggc ctg gac aga gag cac gtg tat gac ctc ttt      530
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69 Ser Met Ala Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe
70         160                 165                 170
72 gag aaa gcc gtg aag gat tac att tgt cct aac att tgg cta gag tat        578
73 Glu Lys Ala Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr
74     175                 180                 185
76 ggc cag tac tca gtt ggt ggg att ggt cag aaa ggt ggc ctt gag aaa        626
77 Gly Gln Tyr Ser Val Gly Gly Ile Gly Gln Lys Gly Gly Leu Glu Lys
78 190                 195                 200                 205
80 gtt cgc tcc gtg ttt gaa agg gct ctc tcg tct gtt ggt tta cat atg        674
81 Val Arg Ser Val Phe Glu Arg Ala Leu Ser Ser Val Gly Leu His Met
82                 210                 215                 220
84 acc aaa gga ctc gcc ctc tgg gag gct tac cga gag ttt gaa agt gcg        722
85 Thr Lys Gly Leu Ala Leu Trp Glu Ala Tyr Arg Glu Phe Glu Ser Ala
86                 225                 230                 235
88 att gtg gaa gct gct cgg ctt gag aaa gtc cac agt ctt ttc cgg cga        770
89 Ile Val Glu Ala Ala Arg Leu Glu Lys Val His Ser Leu Phe Arg Arg
90         240                 245                 250
92 cag ttg gcg atc cca ctc tat gat atg gag gcc aca ttt gca gag tat        818
93 Gln Leu Ala Ile Pro Leu Tyr Asp Met Glu Ala Thr Phe Ala Glu Tyr
94     255                 260                 265
96 gaa gaa tgg tca gaa gac cca ata cca gag tca gta att cag aac tat        866
97 Glu Glu Trp Ser Glu Asp Pro Ile Pro Glu Ser Val Ile Gln Asn Tyr
98 270                 275                 280                 285
100 aac aaa gca cta cag cag ctg gag aaa tat aaa ccc tat gaa gaa gca       914
101 Asn Lys Ala Leu Gln Gln Leu Glu Lys Tyr Lys Pro Tyr Glu Glu Ala
102                 290                 295                 300
104 ctg ttg cag gca gag gca cca agg ctg gca gaa tat caa gca tat atc       962
105 Leu Leu Gln Ala Glu Ala Pro Arg Leu Ala Glu Tyr Gln Ala Tyr Ile
106                 305                 310                 315
108 gat ttt gag atg aaa att ggc gat cct gct cgc att cag ttg atc ttt      1010
109 Asp Phe Glu Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe
110         320                 325                 330
112 gag cgc gcc ctg gtc gag aac tgc ctt gtc cca gac tta tgg atc cgt      1058
113 Glu Arg Ala Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg
114     335                 340                 345
116 tac agt cag tac cta gat cga caa ctg aaa gta aag gat ttg gtt tta      1106
117 Tyr Ser Gln Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu
118 350                 355                 360                 365
120 tct gta cat aac cgc gct att aga aac tgc ccc tgg aca gtt gcc tta      1154
121 Ser Val His Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu
122                 370                 375                 380
124 tgg agt cgg tac ctc ttg gcc atg gag aga cat gga gtt gat cat caa      1202
125 Trp Ser Arg Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln
126                 385                 390                 395
128 gta att tct gta acc ttc gag aaa gct ttg aat gcc ggc ttc atc cag      1250
129 Val Ile Ser Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln
130                 400                 405                 410
132 gcc act gat tat gtg gag att tgg cag gca tac ctt gat tac ctg agg      1298
133 Ala Thr Asp Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg
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134      415                  420                  425
136 aga agg gtt gat ttc aaa caa gac tcc agt aaa gag ctg gag gag ttg      1346
137 Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu
138 430                  435                  440                  445
140 agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa      1394
141 Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu
142                  450                  455                  460
144 gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac      1442
145 Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn
146                  465                  470                  475
148 tgg gct agg att gag gct cga ctg tgc aat aac atg cag aaa gct cgg      1490
149 Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg
150          480                  485                  490
152 gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac      1538
153 Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn
154      495                  500                  505
156 atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag      1586
157 Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln
158 510                  515                  520                  525
160 cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac      1634
161 His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr
162                  530                  535                  540
164 cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt      1682
165 Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly
166          545                  550                  555
168 tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta      1730
169 Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu
170          560                  565                  570
172 gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc      1778
173 Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala
174      575                  580                  585
176 ctt gtg cag caa gaa gaa gaa aag gct gaa caa cgg aaa aga gct cgg      1826
177 Leu Val Gln Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg
178 590                  595                  600                  605
180 gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag      1874
181 Ala Glu Lys Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu
182                  610                  615                  620
184 aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa      1922
185 Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu
186          625                  630                  635
188 gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca      1970
189 Glu Glu Gln Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala
190          640                  645                  650
192 gct gga gaa aca caa aat gta gaa gta gca gca ggg ccc gct ggg aaa      2018
193 Ala Gly Glu Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys
194      655                  660                  665
196 tgt gct gcc gta gat gtg gag ccc cct tcg aag cag aag gag aag gca      2066
197 Cys Ala Ala Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala
198 670                  675                  680                  685
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RAW SEQUENCE LISTING   DATE: 11/25/2001
PATENT APPLICATION: US/09/763,985A   TIME: 14:05:12

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Output Set: N:\CRF3\11212001\I763985A.raw

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200 gcc tcc ctg aag agg gac atg ccc aag gtg ctg cac gac agc agc aag    2114
201 Ala Ser Leu Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys
202             690                 695                 700
204 gac agc atc acc gtc ttt gtc agc aac ctg ccc tac agc atg cag gag    2162
205 Asp Ser Ile Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu
206             705                 710                 715
208 ccg gac acg aag ctc agg cca ctc ttc gag gcc tgt ggg gag gtg gtc    2210
209 Pro Asp Thr Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val
210             720                 725                 730
212 cag atc cga ccc atc ttc agc aac cgt ggg gat ttc cga ggt tac tgc    2258
213 Gln Ile Arg Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys
214     735                 740                 745
216 tac gtg gag ttt aaa gaa gag aaa tca gcc ctt cag gca ctg gag atg    2306
217 Tyr Val Glu Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met
218 750                 755                 760                 765
220 gac cgg aaa agt gta gaa ggg agg cca atg ttt gtt tcc ccc tgt gtg    2354
221 Asp Arg Lys Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val
222             770                 775                 780
224 gat aag agc aaa aac ccc gat ttt aag gtg ttc agg tac agc act tcc    2402
225 Asp Lys Ser Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser
226             785                 790                 795
228 cta gag aaa cac aag ctg ttc atc tca ggc ctg cct ttc tcc tgt act    2450
229 Leu Glu Lys His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr
230             800                 805                 810
232 aaa gag gaa cta gaa gaa atc tgt aag gct cat ggc acc gtg aag gac    2498
233 Lys Glu Glu Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp
234     815                 820                 825
236 ctc agg ctg gtc acc aac cgg gct ggc aaa cca aag ggc ctg gcc tac    2546
237 Leu Arg Leu Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr
238 830                 835                 840                 845
240 gtg gag tat gaa aat gaa tcc cag gcg tcg cag gct gtg atg aag atg    2594
241 Val Glu Tyr Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met
242             850                 855                 860
244 gac ggc atg act atc aaa gag aac atc atc aaa gtg gca atc agc aac    2642
245 Asp Gly Met Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn
246             865                 870                 875
248 cct cct cag agg aaa gtt cca gag aag cca gag acc agg aag gca cca    2690
249 Pro Pro Gln Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro
250             880                 885                 890
252 ggt ggc ccc atg ctt ttg ccg cag aca tac gga gcg agg ggg aag gga    2738
253 Gly Gly Pro Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly
254     895                 900                 905
256 agg acg cag ctg tct cta ctg cct cgt gcc ctg cag cgc cca agt gct    2786
257 Arg Thr Gln Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala
258 910                 915                 920                 925
260 gca gct cct cag gct gag aac ggc cct gcc gcg gct cct gca gtt gcc    2834
261 Ala Ala Pro Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala
262             930                 935                 940
264 gcc cca gca gcc acc gag gca ccc aag atg tcc aat gcc gat ttt gcc    2882
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266             945                 950                 955
268 aag ctg ttt ctg aga aag tgaacgggac gctgggagac aggaaatgcc              2930
269 Lys Leu Phe Leu Arg Lys
270         960
272 ttacttcact ctggcccggc ggacctccca ccacccagca gtgcactggg gatggacagg      2990
274 cctggtgtgc tgcgtgctcg caaccacaga tggctcctcg gctttagaca gaaagggggaa     3050
276 ggggttctaa gtcaagagcc tttcagtgct ccctcatatt gagggcagtg gcagaaaagt      3110
278 gaccactctg caggctgggc ccaggatgtg gtgtcctgag atagttttgt atcttaaaga      3170
280 ctgaggcaca gaagcgaaac gagaacacac tgttttgag acacagttgt ccaaatgttt        3230
282 ctggccagct ccggcccctt tttgtatgac acttctcttc caccctgcac agcacatgtg       3290
284 cccgtcattc ttttaatttt aaaagatgaa atggcagatg ctagtaattc acagaatggc      3350
286 ctcttgtggg ggtgggtctg agggaagtca gctataaaac atttgctgga gttttgttca      3410
288 atggggctgt gcatttttat attatgtgtt tgtaaatgac atgtcagccc ttgtttcatg      3470
290 tttcctaaaa gcagaatatt tgcaacattt gttttgtata ggaattattt gtgccacctg      3530
292 ctgtggactg ttttctttgc ctagtgacta gtgacctgtg ttgtctaaac atgagtttca      3590
294 gcccttgtt tttgtttaat accatgtcaa atgcaaactt caattctccc catttagctt        3650
296 tattaaactg acgttctctt caaaacttct tgctgaatgg tactcagatg tgcattcaca      3710
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305 <212> TYPE: PRT
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318 Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala Ala Thr Tyr
319         35                  40                  45
322 Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu
323     50                  55                  60
326 Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro
327 65                  70                  75                  80
330 Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Lys Asn Gln Leu
331             85                  90                  95
334 Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr
335             100                 105                 110
338 Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu
339         115                 120                 125
342 Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu
343     130                 135                 140
346 Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile Ser Met Ala
347 145                 150                 155                 160
350 Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe Glu Lys Ala
351             165                 170                 175
354 Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr Gly Gln Tyr
355             180                 185                 190
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VERIFICATION SUMMARY   DATE: 11/25/2001
PATENT APPLICATION: US/09/763,985A   TIME: 14:05:14

Input Set : **A:\0020-4817P.ST25.txt**
Output Set: **N:\CRF3\11212001\I763985A.raw**

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L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
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